

Constitutive expression of *MKS1* confers susceptibility to *Botrytis cinerea* infection independent of *PAD3* expression

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Key words: Arabidopsis, MAPK cascade, innate immune response, *Botrytis cinerea*, lesion mimic mutant, resistance genes, transcription

Abbreviations: SA, salicylic acid; *B. cinerea*, *Botrytis cinerea*; *Pst* DC3000, *Pseudomonas syringae* pv tomato DC3000; MAPK, mitogen activated protein kinase; R-gene, resistance genes; JA, jasmonate

Signal transduction through MAPK cascades is essential for eukaryotic cell response to various extracellular stimuli, such as the induction of innate immune responses. *Arabidopsis thaliana* relies in particular on three of its 20 MAPKs, MPK3, -4, -6, for a proper immune response. Recently we showed that one MPK4-substrate, MKS1, is required for basal resistance against the virulent *Pseudomonas syringae* and the oomycete *Hyaloperonospora arabidopsidis*. Overexpression of MKS1 (35S-MKS1) led to increased resistance to the same pathogens but also to an increased susceptibility toward the fungi *Botrytis cinerea*. MKS1 interacts with the transcription factor WRKY33, which in turn controls the regulation of *PAD3* and *CYP71A13*, two genes, required for proper resistance to *B. cinerea*. Therefore, we tested if the increased susceptibility toward *B. cinerea* from 35S-MKS1 was due to deregulation of WRKY33 targets. *PAD3* and *CYP71A13* expression is similar in 35S-MKS1 and WT after *B. cinerea* treatment suggesting another mechanism controls 35S-MKS1 susceptibility.

MPK4 is part of a signaling cascade that consists of MEKK1 and MKK1/MKK2. Deletion mutants of *mek1*,^{1,2} *mkk1/mkk2*,³ double knockout and *mpk4*,⁴ share a dwarf phenotype and MEKK1 and MKK1/MKK2 are required for proper MPK4 activation.¹⁻³ MKS1 was identified in a yeast-two-hybrid screen for interactors of MPK4 and found to be an MPK4 substrate and in vivo partner.⁵ Importantly, deletion of *MKS1* abrogates some of the *mpk4* phenotypes.^{6,7}

We recently found that MPK4-MKS1-WRK33 exist in a nuclear localized complex. Activation of MPK4, for example by bacterial elicitors, leads to MKS1 phosphorylation and dissociation of WRKY33 from MPK4 complexes. Subsequently, WRKY33 binds to the promoter of *PAD3* and promote its expression.⁷ A recent publication confirmed that WRKY33 binds the *PAD3* promoter.⁸ In addition, Mao et al. find that WRKY33 is a substrate of especially MPK6 and to a lower extent MPK3 and MPK4 (most strongly in the absence of MPK3 and MPK6).⁸

Expression of *PAD3* and *CYP71A13* is required for the production of the antimicrobial compound camalexin, necessary for proper defense against *B. cinerea*.⁹ Because overexpression of *MKS1* leads to increased susceptibility to *B. cinerea*⁶ and MKS1 and WRKY33 interact in planta and are regulated by MAPK activity, it is possible that 35S-MKS1 susceptibility is caused by deregulation of WRKY33 targets.

We therefore tested the expression of the WRKY33 targets *PAD3* and *CYP71A13* in *Ler* (wild type control), 35S-MKS1, *mks1* and *mpk4* before and 48 h after infection with *B. cinerea*. Interestingly, there was no difference in the expression of these two genes between 35S-MKS1 and wild type (Fig. 1). In accordance with previously published data, *mpk4* accumulates *PAD3* and *CYP71A13* transcripts even in absence of infection.^{5,7}

Since MPK4 is activated within minutes and releases WRKY33 to bind the promoter of *PAD3* within hours and not days, we tested whether a difference in the early response to *B. cinerea* might explain the different susceptibilities. Real time PCR on cDNA from RNA extracted at time points between 2–12 h after *B. cinerea* treatment did not reveal a strong consistent differential response in 35S-MKS1 compared with *Ler* and *mks1* (data not shown).

It is perhaps not surprising that expression of the 35S-MKS1 construct does not lead to reduced *PAD3* and *CYP71A13*. The model proposed by Qiu et al.⁷ would project that excess MKS1 leads to less WRKY33 sequestered in a complex with MPK4. With recent results from Mao et al. one might suspect more WRKY33 to be readily available for MPK3,(4),6 phosphorylation. However, we do not see consistently higher *PAD3*, *CYP71A13* transcript levels upon induction in 35S-MKS1. Moreover higher levels of *PAD3*, *CYP71A13* in 35S-MKS1 would not explain its susceptibility phenotype.

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Submitted: 05/24/11; Revised: 06/22/11; Accepted: 06/22/11
DOI: 10.4161/psb.6.10.16759

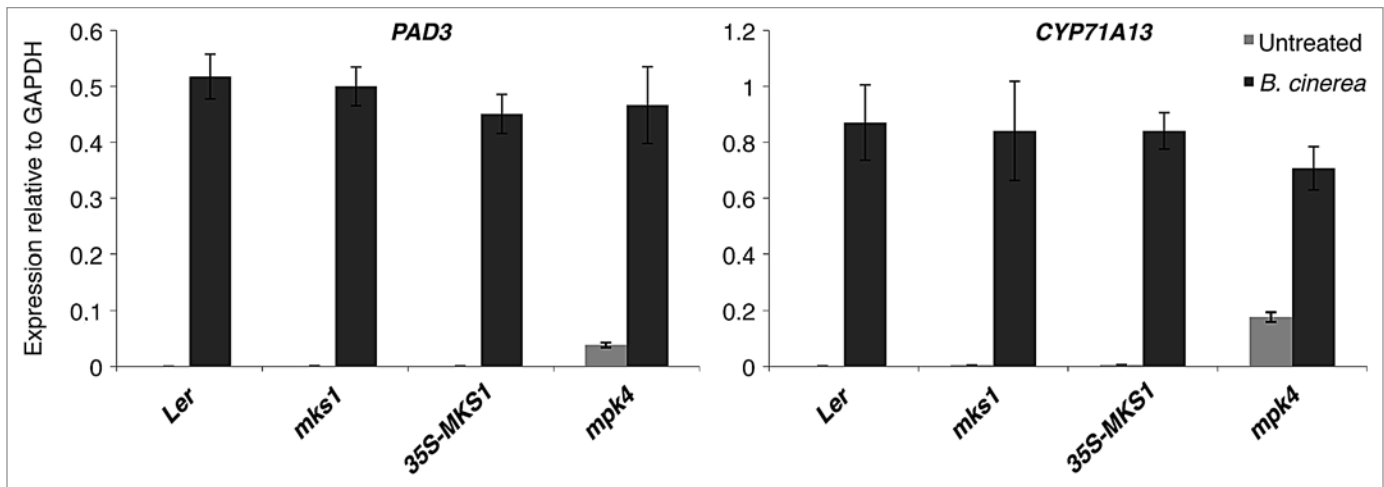


Figure 1. Real-time PCR detection of PAD3 and CYP71A13 on untreated controls or plants treated with *B. cinerea* for 48 h. Samples were tested in triplicate and normalized to GAPDH. Means \pm SD is shown.

Like constitutive-defense/lesion-mimic mutants, *35S-MKS1* plants are semi-dwarfed with occasional lesions, accumulate *PRI* transcript accompanied with increased levels of the plant hormone salicylic acid (SA) and exhibit increased resistance toward *Pseudomonas syringae* pv. tomato DC3000.^{5,6}

Although important, camalexin is not the only determinant in *B. cinerea* susceptibility.¹⁰ Other factors include e.g., JA/ethylene signaling.¹¹ Methyl-JA treatment of *35S-MKS1* leads to increased levels of the JA marker gene *PDFI.2*.⁵ Although *PDFI.2* induction appears to be slightly impaired upon *B. cinerea* infection⁶ there is no block in JA/ethylene signaling and this modest decrease is probably not the reason for the enhanced susceptibility.

It has been observed that induction of cell death through the hypersensitive response can facilitate *B. cinerea* infection.¹² This suggests that the lesions sometimes observed in *35S-MKS1* might be the cause of the enhanced susceptibility and that perhaps the susceptibility is an indirect effect. *Suppressor of salicylic acid insensitive 2 (ssi2)* is a lesion-mimic and *B. cinerea*-susceptible mutant. *SSI2* encodes a stearyl-ACP desaturase.¹³ Additionally, like *35S-MKS1*, *ssi2* is smaller than wild type, accumulates *PRI* transcript

and shows enhanced resistance to virulent strains of *Pseudomonas syringae*.^{13,14} Surprisingly, *B. cinerea* susceptibility in *ssi2* seems to be independent of its lesions. The double mutants *ssi2/pad4* and *ssi2/eds5* partially rescue *ssi2* size but still have spontaneous cell death and are much more resistant to *B. cinerea* than the single mutant.¹⁴

The *ssi2* mutant has low levels of oleic acid (18:1) and its phenotype can be rescued by addition of oleic acid. Recently, it has been shown that the low levels of oleic acid leads to induction of Resistance-gene (R-gene) expression dependent on EDS1 and SA production (through SID2).^{15,16} The authors propose that the accumulation of various R-genes and activation thereof is responsible for *ssi2* altered defense-related phenotype.

Whether *35S-MKS1*-phenotype is due to aberrant R-gene activation remains to be tested. If R-gene activation causes both the *35S-MKS1* and *ssi2* phenotypes presumably the properties of the specifically activated R-gene(s) result in their secondary phenotypes such as *B. cinerea* susceptibility.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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